

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/485,163

1812

DATE: 10/29/97
TIME: 15:37:02

INPUT SET: S21268.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Beaudry, Gary A.
Maddon, Paul J.

(ii) TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.24

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/485,163
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US

(viii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 278-0400
(B) TELEFAX: (212) 391-0525
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

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47 (D) TOPOLOGY: unknown
48
49 (ii) MOLECULE TYPE: peptide
50
51 (vi) ORIGINAL SOURCE:
52 (A) ORGANISM: homo sapien
53 (G) CELL TYPE: lymphocyte
54
55
56
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59 Phe Glu Arg Lys Cys Cys Val Gln Cys Pro Pro Cys Asp
60 1 5 10
61

62 (2) INFORMATION FOR SEQ ID NO:2:
63
64 (i) SEQUENCE CHARACTERISTICS:
65 (A) LENGTH: 1796 base pairs
66 (B) TYPE: nucleic acid
67 (C) STRANDEDNESS: double
68 (D) TOPOLOGY: unknown
69
70 (ii) MOLECULE TYPE: cDNA
71
72 (vi) ORIGINAL SOURCE:
73 (A) ORGANISM: Homo sapiens
74 (G) CELL TYPE: Lymphocyte
75
76
77

78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
79
80 CAAGCCCAGA GCCCTGCCAT TTCTGTGGGC TCAGGTCCCT ACTGCTCAGC CCCTTCCTCC 60
81
82 CTCGGCAAGG CCACAATGAA CCGGGGAGTC CCTTTTAGGC ACTTGCTTCT GGTGCTGCAA 120
83
84 CTGGCGCTCC TCCCAGCAGC CACTCAGGGA AAGAAAGTGG TGCTGGGCAA AAAAGGGGAT 180
85
86 ACAGTGGAAC TGACCTGTAC AGCTTCCCAG AAGAAGAGCA TACAATTCCA CTGGAAAAAC 240
87
88 TCCAACCAGA TAAAGATTCT GGGAAATCAG GGCTCCTTCT TAACTAAAGG TCCATCCAAG 300
89
90 CTGAATGATC GCGCTGACTC AAGAAGAAGC CTTTGGGACC AAGGAAACTT CCCCCTGATC 360
91
92 ATCAAGAATC TTAAGATAGA AGACTCAGAT ACTTACATCT GTGAAGTGGA GGACCAGAAG 420
93
94 GAGGAGGTGC AATTGCTAGT GTTCGGATTG ACTGCCAACT CTGACACCCA CCTGCTTCAG 480
95
96 GGGCAGAGCC TGACCCTGAC CTTGGAGAGC CCCCCTGGTA GTAGCCCCTC AGTGCAATGT 540
97
98 AGGAGTCCAA GGGGTAAAAA CATACAGGGG GGAAGACCC TCTCCGTGTC TCAGCTGGAG 600
99

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101
102 AAAATAGACA TCGTGGTGCT AGCTTTCGAG CGCAAATGTT GTGTGAGTG CCCACCGTGC 720
103
104 CCAGGTAAGC CAGCCCAGGC CTCGCCCTCC AGCTCAAGGC GGGACAGGTG CCCTAGAGTA 780
105
106 GCCTGCATCC AGGGACAGGC CCCAGCTGGG TGCTGACACG TCCACCTCCA TCTCTTCCTC 840
107
108 AGCACCACCT GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CAAAAACCCA AGGACACCCT 900
109
110 CATGATCTCC CGGACCCCTG AGGTCACGTG CGTGGTGGTG GACGTGAGCC ACGAAGACCC 960
111
112 CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG CATAATGCCA AGACAAAGCC 1020
113
114 ACGGGAGGAG CAGTTCAACA GCACGTTCCG TGTGGTCAGC GTCCTCACCG TTGTGCACCA 1080
115
116 GGACTGGCTG AACGGCAAGG AGTACAAGTG CAAGGTCTCC AACAAAGGCC TCCAGCCCCC 1140
117
118 CATCGAGAAA ACCATCTCCA AAACCAAAGG TGGGACCCGC GGGGTATGAG GGCCACATGG 1200
119
120 ACAGAGGCCG GCTCGGCCCA CCCTCTGCCC TGGGAGTGAC CGCTGTGCCA ACCTCTGTCC 1260
121
122 CTACAGGGCA GCCCCGAGAA CCACAGGTGT ACACCCTGCC CCCATCCCCG GAGGAGATGA 1320
123
124 CCAAGAACCA GGTACGCCTG ACCTGCCTGG TCAAAGGCTT CTACCCCAGC GACATCGCCC 1380
125
126 TGGAGTGGGA GAGCAATGGG CAGCCGGAGA ACAACTACAA GACCACACCT CCCATGCTGG 1440
127
128 ACTCCGACGG CTCCTTCTTC CTCTACAGCA AGCTCACCGT GGACAAGAGC AGGTGGCAGC 1500
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130 AGGGGAACTG CTTCTCATGC TCCGTGATGC ATGAGGCTCT GCACAACCAC TACACGCAGA 1560
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132 AGAGCCTCTC CCTGTCTCCG GGTAAATGAG TGCCACGGCC GGCAAGCCCC CGCTCCCCAG 1620
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134 GCTCTCGGGG TCGCGTGAGG ATGCTTGGA CGTACCCCGT GTACATACTT CCCAGGCACC 1680
135
136 CAGCATGGAA ATAAAGCACC CAGCGCTGCC CTGGGCCCCCT GCGAGACTGT GATGGTTCTT 1740
137
138 TCCGTGGGTC AGGCCGAGTC TGAGGCCTGA GTGGCATGAG GGAGGCAGAG TGGGTC 1796
139
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapien
- (G) CELL TYPE: lymphocyte

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153
154
155
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
157
158 Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
159 1 5 10 15
160
161
162 Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
163 20 25 30
164
165
166 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
167 35 40 45
168
169
170 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
171 50 55 60
172
173
174 Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
175 65 70 75 80
176
177
178 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
179 85 90 95
180
181
182
183 Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
184 100 105 110
185
186
187 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
188 115 120 125
189
190
191 Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
192 130 135 140
193
194
195 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
196 145 150 155 160
197
198 Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
199 165 170 175
200
201
202 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
203 180 185 190
204
205

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206		Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Glu	Arg	Lys	Cys
207				195					200								205
208																	
209																	
210	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	
211		210					215					220					
212																	
213																	
214	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	
215	225					230					235						240
216																	
217	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	
218					245					250					255		
219																	
220																	
221	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	
222				260					265					270			
223																	
224																	
225	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	
226			275					280					285				
227																	
228																	
229	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	
230		290					295					300					
231																	
232																	
233	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	
234	305					310					315					320	
235																	
236	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	
237					325					330					335		
238																	
239																	
240	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	
241				340					345					350			
242																	
243																	
244	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	
245			355					360					365				
246																	
247																	
248	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	
249		370					375</										

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SEQUENCE VERIFICATION REPORT
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Original Text